DEC 27 2005 W

SEQUENCE LISTING Max-Planck-Gesellschaft z. Förd. d. Wissenschaften <120> Plants With Modified Gene Expression <130> DEBE:005US <140> 10/030,386 <140> 2002-01-02 <150> PCT/DE00/02233 <151> 2000-07-03 <150> DE 199 30 570.6 <151> 1999-07-02 <160> 8 <170> PatentIn Ver. 2.1 <210> 1 <211> 3389 <212> DNA <213> Arabidopsis thaliana <400> 1 actagttgac cacatgaact aaacttcttg gacaatcatc aatggacaca tgttagcttt 60 gatttgctgt gaatttgttt tatctctcag tataattatc actttcttgt ttatgcttac 120 aatatatttt atggtttaga gttttgtttt acgattttgg atttaatgga taaagattag 180 ggattgaggg tttgagttta gggtaaggaa attaggcttt agtgtagagt ctcaagggtt 240 taaqqtttac acaccacaaa ccatttqctt qtqtcaacaa cattqtatca tattttcaaa 300 aaaattttqt tqaaqqacct tqtattqata tatataaaqc gaactqtttq qataaqttta 360 tgtggacaat atatattgga tacataatta gaaacatagt ttaatatctg atatttgttg 420 ggaatatata atactactta ggtttaaata tatagtattt catatgatgc gaactgtttg 480 gataagttta cgtggacaat atatatttga tacataatta ggaacatagt ttaatatttg 540 atatttgttg ggaatatata attctactta cgcttaaata tttttatttg aattaaagca 600 tttcatataa tgtgaactgt ttgaatatgt ttacatggac aatatatatt ggatacataa 660 ttaggaacat agtttaatat ctgatatttg ttggaaatat ataatattag ttaagcttaa 720 atatttttat ttgatataat atttgactta aacattttta tttgattaaa ctaaatttta 780 acagatetta ecattaattt ttaaettgtt atetetatet aatgteaegt atattgtttt 840 ttagtaattg gcaacaaaat taatttatct cctgtttttt ttccttctca cctttataag 900 ggtaaaatgg tcataaaatc agtaaaaaag gtggaaaagt gcccactccc tcaaaagtgt 960 cataaacgtc caaactttct ccataaatgc cttattttgg aacattccat atagattata 1020 acttattata ggttataact tattatagtt acgttaatta tatgaatttc tattagttat 1080 cacacaatca aatattttaa tcacaaaaat ttattaaaca tttttatatgt ggtagtataa 1140 tgcaataaca tattatatgt ggtggcataa tgcaacaaca tattatttgt ctacgaatct 1200 cctttatttt tcgtttatgt aacaacagta aaacggattg tttagcttga tattctatat 1260 tataataatc taaagttatt tttgtaaatt atttttttc caaattggat aaccaatcat 1320

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Asp Arg Ile Asn Leu Asn Ser Asn Leu Asp Leu Asn Pro Asn Pro Leu 50 55 60

Arg Glu Val Asp Val Asp Leu His Ile Gly Leu Pro Gly Phe Gly Lys
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Pro Ser Asn Asp Ala Lys Gln Leu Lys Lys Arg Asn Gly Lys Glu Ile 100 105 110

Ala Thr Tyr Asp Ala Gly Lys Gly Ile Glu Asn Glu Leu Ser Gly Lys
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Ala Tyr Trp Ile Pro Ala Pro Glu Gln Ile Leu Ile Gly Phe Thr His 130 135 140

Phe Ser Cys His Val Cys Phe Lys Thr Phe Asn Arg Tyr Asn Asn Leu 145 150 155 160

Gln Met His Met Trp Gly His Gly Ser Gln Tyr Arg Lys Gly Pro Glu 165 170 175

Ser Leu Lys Gly Thr Gln Pro Arg Ala Met Leu Gly Ile Pro Cys Tyr 180 185 190

Cys Cys Val Glu Gly Cys Arg Asn His Ile Asp His Pro Arg Ser Lys 195 200 205

Pro Leu Lys Asp Phe Arg Thr Leu Gln Thr His Tyr Lys Arg Lys His 210 215 220

Gly His Lys Pro Phe Ser Cys Arg Leu Cys Gly Lys Leu Leu Ala Val 225 230 235 240

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Asn Ile Asp His Pro Arg Ala Lys Pro Leu Lys Asp Phe Arg Thr Leu

275 280 285

Gln Thr His Tyr Lys Arg Lys His Gly Ile Lys Pro Phe Met Cys Arg 290 295 300

Lys Cys Gly Lys Ala Phe Ala Val Arg Gly Asp Trp Arg Thr His Glu 305 310 315 320

Lys Asn Cys Gly Lys Leu Trp Tyr Cys Ile Cys Gly Ser Asp Phe Lys 325 330 335

His Lys Arg Ser Leu Lys Asp His Ile Lys Ala Phe Gly Asn Gly His 340 345 350

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Ser Cys Leu Leu Leu Phe Phe Ser Leu Ser Ser Leu Leu Lys Leu 50 55 60

Met Ala Asp Pro Asp Cys Ile Phe Arg Asn Gly Tyr Val Asp Tyr Tyr
65 70 75 80

Asn Tyr Ser Phe Asn Tyr Ala Thr Ser Leu Ser Arg Ile Tyr Asn Ser 85 90 95

His Asp Ser Phe Phe Phe Phe Pro Gln Ser Gly Asp Leu Arg Arg Pro 100 105 110

Pro Pro Pro Pro Thr Pro Pro Pro Ser Pro Pro Leu Arg Glu Ala Leu
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Pro Leu Leu Ser Leu Ser Pro Ala Asn Thr Gln Gln Asp His His 130 135 140

Asn His Asp His Leu Ile Gln Glu Pro Pro Ser Thr Ser Met Asp Val 145 150 155 160

Asp Tyr Asp His His Gln Asp Asp His His Asn Leu Asp Asp Asp 165 170 175

Asp His Asp Val Thr Val Ala Leu His Ile Gly Leu Pro Ser Pro Ser 180 185 190

Ser Arg Thr Thr His His Glu Asp Met Asn His Lys Lys Asp Leu 210 215 220

Asp His Glu Tyr Ser His Gly Ala Val Gly Gly Glu Asp Asp Asp 225 230 235 240

Glu Asp Ser Val Gly Gly Asp Gly Gly Cys Arg Ile Ser Arg Leu Asn 245 250 255

Lys Gly Gln Tyr Trp Ile Pro Thr Pro Ser Gln Ile Leu Ile Gly Pro
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Thr Gln Phe Ser Cys Pro Val Cys Phe Lys Thr Phe Asn Arg Tyr Asn 275 280 285

Asn Met Gln Met His Met Trp Gly His Gly Ser Gln Tyr Arg Lys Gly 290 295 300

Pro Glu Ser Leu Arg Gly Thr Gln Pro Thr Gly Met Leu Arg Leu Pro 305 310 315 320

Cys Tyr Cys Cys Ala Pro Gly Cys Arg Asn Asn Ile Asp His Pro Arg 325 330 335

Ala Lys Pro Leu Lys Asp Phe Arg Thr Leu Gln Thr His Tyr Lys Arg 340 345 350

Lys His Gly Ile Lys Pro Phe Met Cys Arg Lys Cys Gly Lys Ala Phe 355 360 365

Ala Val Arg Gly Asp Trp Arg Thr His Glu Lys Asn Cys Gly Lys Leu 370 375 380

Trp Tyr Cys Ile Cys Gly Ser Asp Phe Lys His Lys Arg Ser Leu Lys 385 390 395 400

Asp His Ile Lys Ala Phe Thr Asn Gly His Gly Ala Tyr Gly Ile Asp
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Gly Ser Tyr Tyr Ser Asn Thr Thr Asn Pro Asn Tyr Ile Asn His
35 40 45

Thr His Thr Thr Ser Thr Ser Pro Asn Ser Pro Pro Leu Arg Glu Ala 50 55 60

Leu Pro Leu Leu Ser Leu Ser Pro Ile Arg His Gln Gln Gln Asp
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Gln His Tyr Phe Met Asp Thr His Gln Ile Ser Ser Ser Asn Phe Leu 85 90 95

Asp Asp Pro Leu Val Thr Val Asp Leu His Leu Gly Leu Pro Asn Tyr
100 105 110

Gly Val Gly Glu Ser Ile Arg Ser Asn Ile Ala Pro Asp Ala Thr Thr 115 120 125

Asp Glu Gln Asp Gln Asp His Asp Arg Gly Val Glu Val Thr Val Glu
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Ser His Leu Asp Asp Asp Asp Asp His His Gly Asp Leu His Arg Gly 145 150 155 160

His His Tyr Trp Ile Pro Thr Pro Ser Gln Ile Leu Ile Gly Pro Thr
165 170 175

Gln Phe Thr Cys Pro Leu Cys Phe Lys Thr Phe Asn Arg Tyr Asn Asn 180 185 190

Met Gln Asn Asn Ile Asp His Pro Arg Ala Lys Pro Leu Lys Asp Phe 195 200 205 Arg Thr Leu Gln Thr His Tyr Lys Arg Lys His Gly Ser Lys Pro Phe 210 215 220

Ala Cys Arg Met Cys Gly Lys Ala Phe Ala Val Lys Gly Asp Trp Arg 225 230 235 240

Thr His Glu Lys Asn Cys Gly Lys Leu Trp Tyr Cys Ser Cys Gly Ser 245 250 255

Asp Phe Lys His Lys Arg Ser Leu Lys Asp His Val Lys Ala Phe Gly 260 265 270

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Cys Ala Ala Gly Cys Arg Asn Ser Val Ser His Pro Arg Ala Arg Pro 35 40 45

Leu Lys Asp Phe Arg Thr 50